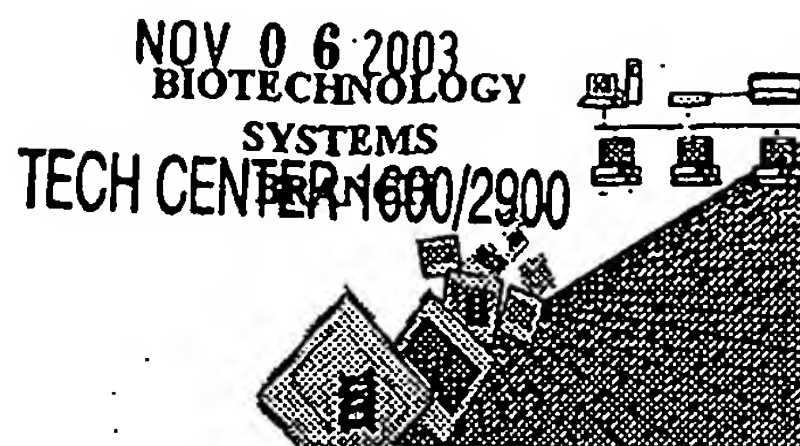




RECEIVED



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/009,792B  
Source: 1600  
Date Processed by STIC: 10/23/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/2003):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/2003



## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/009,792B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."  
    Wrapped Aminos
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.  
    Numbering
- 4      Non-ASCII    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length    Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.  
    "bug"
- 7      Skipped Sequences    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (OLD RULES)    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    This sequence is intentionally skipped
- Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    (NEW RULES)    <210> sequence id number  
                    <400> sequence id number  
                    000
- 9      Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    (NEW RULES)    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
    Response    scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>    Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                    (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.  
    "bug"
- 13      Misuse of n/Xaa    "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



1600

## RAW SEQUENCE LISTING

DATE: 10/23/2003

PATENT APPLICATION: US/10/009,792B

TIME: 11:13:03

Input Set : A:\hylee60seq1.txt

Output Set: N:\CRF4\10232003\J009792B.raw

4 <110> APPLICANT: LEE, Sang-Yup  
 5       JEONG, Ki-Jun  
 7 <120> TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN  
 8       GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)  
 11 <130> FILE REFERENCE: HYLEE60.001APC  
 13 <140> CURRENT APPLICATION NUMBER: US 10/009,792B  
 14 <141> CURRENT FILING DATE: 2001-12-13  
 16 <150> PRIOR APPLICATION NUMBER: PCT/KR01/00549  
 17 <151> PRIOR FILING DATE: 2001-03-31  
 19 <150> PRIOR APPLICATION NUMBER: KR 10-2000-0017052  
 20 <151> PRIOR FILING DATE: 2000-03-31  
 22 <160> NUMBER OF SEQ ID NOS: 30  
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0

## ERRORED SEQUENCES

402 <210> SEQ ID NO: 30  
 403 <211> LENGTH: 14  
 404 <212> TYPE: PRT  
 405 <213> ORGANISM: synthetic sequence  
 407 <400> SEQUENCE: 30  
 408 Ala Gly Pro His His His His His Ile Glu Gly Arg Thr  
 409   1                               5                               10  
 E--> 413 S:\DOCS\SGJ\HYLEE60-SL.TXT  
 E--> 414 100903  
 E--> 415 1  
 E--> 418 9

pp 1-2  
 Does Not Comply  
 Corrected Diskette Needed

invalid  
 response - see item 10 on Error Summary  
 Sheet

(this error  
 also appears  
 in sequences  
 28-29)

all P 2, too



10/009,792B 2

<210> 1  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Oligopeptide

*give source of genetic material - see item 11*

*on Enov*

*Summary Sheet*

<400> 1

Ala Gly Pro His His His His His His Ile Glu Gly Arg  
1 5 10



VERIFICATION SUMMARY

PATENT APPLICATION: US/10/009,792B

DATE: 10/23/2003

TIME: 11:13:04

Input Set : A:\hylee60seq1.txt

Output Set: N:\CRF4\10232003\J009792B.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:413 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:413 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
L:414 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:30  
M:332 Repeated in SeqNo=30  
L:418 M:252 E: No. of Seq. differs, <211> LENGTH:Input:14 Found:15 SEQ:30